



1

SEQUENCE LISTING

<110> HAMILTON, STEPHEN

<120> ENDOMANNOSIDASES IN THE MODIFICATION OF GLYCOPROTEINS
IN EUKARYOTES

<130> GFI/109 CIP

<140> 10/695,243

<141> 2003-10-27

<150> 10/371,877

<151> 2003-02-20

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<170> PatentIn Ver. 3.2

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<212> DNA

<213> Homo sapiens

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<221> CDS

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cta ttt att ttc tct ctg atg atg ggt tta aaa atg ctg aga cca aat	96
Leu Phe Ile Phe Ser Leu Met Met Gly Leu Lys Met Leu Arg Pro Asn	
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aca gct act ttt gga gct cct ttt gga ctt gac ctt ctt cca gaa ctt	144
Thr Ala Thr Phe Gly Ala Pro Phe Gly Leu Asp Leu Leu Pro Glu Leu	
35 40 45	

cat caa cga act att cat ttg ggg aaa aat ttt gat ttc caa aag agt	192
His Gln Arg Thr Ile His Leu Gly Lys Asn Phe Asp Phe Gln Lys Ser	
50 55 60	

gac aga atc aac agt gaa aca aat acc aag aat tta aaa agt gtt gaa	240
Asp Arg Ile Asn Ser Glu Thr Asn Thr Lys Asn Leu Lys Ser Val Glu	
65 70 75 80	

atc act atg aaa cct tcc aaa gcc tct gaa ctt aac ttg gat gaa cta	288
Ile Thr Met Lys Pro Ser Lys Ala Ser Glu Leu Asn Leu Asp Glu Leu	
85 90 95	

cca	cct	ctg	aac	aat	tat	cta	cat	gta	ttt	tat	tac	agt	tgg	tat	gga	336
Pro	Pro	Leu	Asn	Asn	Tyr	Leu	His	Val	Phe	Tyr	Tyr	Ser	Trp	Tyr	Gly	
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Glu	His	Trp	Asp	Pro	Arg	Ile	Ala	Lys	Asn	Tyr	Pro	Gln	Gly	Arg	His	
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Tyr	Ser	Ser	Arg	Asp	Pro	Ser	Val	Ile	Glu	Thr	His	Met	Arg	Gln	Met	
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Val	Asn	Asp	Glu	Asn	Gly	Glu	Pro	Thr	Asp	Asn	Leu	Val	Pro	Thr	Ile	
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Thr	Lys	Pro	Glu	Lys	Trp	Ala	Asn	Leu	Leu	Thr	Thr	Ser	Gly	Ser	Arg	
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 Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly Ser Ser His Gln
 325 330 335
 aat tgg gct agc cta aaa tta att tgt gat aaa tac aac tta ata ttt 1056
 Asn Trp Ala Ser Leu Lys Leu Ile Cys Asp Lys Tyr Asn Leu Ile Phe
 340 345 350
 atc cca agt gtg ggc cca gga tac ata gat acc agc atc cgt cca tgg 1104
 Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr Ser Ile Arg Pro Trp
 355 360 365
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 Asn Thr Gln Asn Thr Arg Asn Arg Ile Asn Gly Lys Tyr Tyr Glu Ile
 370 375 380
 ggt ctg agt gcc gca ctt cag aca cgc ccc agc tta att tct atc acc 1200
 Gly Leu Ser Ala Ala Leu Gln Thr Arg Pro Ser Leu Ile Ser Ile Thr
 385 390 395 400
 tct ttt aat gag tgg cat gaa gga act cag att gaa aaa gct gtt ccc 1248
 Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu Lys Ala Val Pro
 405 410 415
 aaa aga acc agt aat aca gtg tac cta gat tac cgt cct cat aaa cca 1296
 Lys Arg Thr Ser Asn Thr Val Tyr Leu Asp Tyr Arg Pro His Lys Pro
 420 425 430
 ggt ctt tac cta gaa ctg act cgc aag tgg tct gaa aaa tac agt aag 1344
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 gaa aga gca act tat gca tta gat cgc cag ctg cct gtt tct taa 1389
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Thr Ala Thr Phe Gly Ala Pro Phe Gly Leu Asp Leu Leu Pro Glu Leu
 35 40 45
 His Gln Arg Thr Ile His Leu Gly Lys Asn Phe Asp Phe Gln Lys Ser
 50 55 60
 Asp Arg Ile Asn Ser Glu Thr Asn Thr Lys Asn Leu Lys Ser Val Glu
 65 70 75 80
 Ile Thr Met Lys Pro Ser Lys Ala Ser Glu Leu Asn Leu Asp Glu Leu
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 Pro Pro Leu Asn Asn Tyr Leu His Val Phe Tyr Tyr Ser Trp Tyr Gly
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 Asn Pro Gln Phe Asp Gly Lys Tyr Ile His Trp Asn His Pro Val Leu
 115 120 125
 Glu His Trp Asp Pro Arg Ile Ala Lys Asn Tyr Pro Gln Gly Arg His
 130 135 140
 Asn Pro Pro Asp Asp Ile Gly Ser Ser Phe Tyr Pro Glu Leu Gly Ser
 145 150 155 160
 Tyr Ser Ser Arg Asp Pro Ser Val Ile Glu Thr His Met Arg Gln Met
 165 170 175
 Arg Ser Ala Ser Ile Gly Val Leu Ala Leu Ser Trp Tyr Pro Pro Asp
 180 185 190
 Val Asn Asp Glu Asn Gly Glu Pro Thr Asp Asn Leu Val Pro Thr Ile
 195 200 205
 Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val Thr Phe His Ile Glu
 210 215 220
 Pro Tyr Ser Asn Arg Asp Asp Gln Asn Met Tyr Lys Asn Val Lys Tyr
 225 230 235 240
 Ile Ile Asp Lys Tyr Gly Asn His Pro Ala Phe Tyr Arg Tyr Lys Thr
 245 250 255
 Lys Thr Gly Asn Ala Leu Pro Met Phe Tyr Val Tyr Asp Ser Tyr Ile
 260 265 270
 Thr Lys Pro Glu Lys Trp Ala Asn Leu Leu Thr Thr Ser Gly Ser Arg
 275 280 285
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cta ttt att ttt tct ctg atg atg ggc tta aag atg ctg tgg cca aac
Leu Phe Ile Phe Ser Leu Met Met Gly Leu Lys Met Leu Trp Pro Asn
      20              25              30

gca gca tcc ttt gga cct cct ttt gga ctt gac ctc ctt cca gaa ctt
Ala Ala Ser Phe Gly Pro Pro Phe Gly Leu Asp Leu Leu Pro Glu Leu
      35              40              45

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cta	ttt	att	ttt	tct	ctg	atg	atg	ggc	tta	aag	atg	ctg	tgg	cca	aac	96
Leu	Phe	Ile	Phe	Ser	Leu	Met	Met	Gly	Leu	Lys	Met	Leu	Trp	Pro	Asn	
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His	Pro	Leu	Asn	Ala	His	Ser	Gly	Asn	Lys	Ala	Asp	Phe	Gln	Arg	Ser	
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Ser	Arg	Asp	Asp	Asn	Gly	Glu	Ala	Thr	Asp	His	Leu	Val	Pro	Thr	Ile	
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Ile	Ile	Asp	Lys	Tyr	Gly	Asn	His	Pro	Ala	Phe	Tyr	Arg	Tyr	Lys	Thr	
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agt gtt cgc agt tct ctt tat gat gga ttg ttt att gca ctt cta gta	912
Ser Val Arg Ser Ser Leu Tyr Asp Gly Leu Phe Ile Ala Leu Leu Val	
290 295 300	
gaa gaa aag cat aaa aat gat att ctt cag agt ggt ttt gat ggt att	960
Glu Glu Lys His Lys Asn Asp Ile Leu Gln Ser Gly Phe Asp Gly Ile	
305 310 315 320	
tac aca tat ttt gcc aca aat ggc ttt aca tat ggc tca tct cat cag	1008
Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly Ser Ser His Gln	
325 330 335	
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Asn Trp Asn Asn Leu Lys Ser Phe Cys Glu Lys Asn Asn Leu Met Phe	
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Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr Ser Ile Arg Pro Trp	
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370 375 380	
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Gly Leu Ser Ala Ala Leu Gln Thr His Pro Ser Leu Ile Ser Ile Thr	
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Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu Lys Ala Val Pro	
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420 425 430	
agt ctt tat cta gaa cta act cga aag tgg tct gaa aaa ttc agt aag	1344
Ser Leu Tyr Leu Glu Leu Thr Arg Lys Trp Ser Glu Lys Phe Ser Lys	
435 440 445	
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<212> PRT

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Ala	Ala	Ser	Phe	Gly	Pro	Pro	Phe	Gly	Leu	Asp	Leu	Leu	Pro	Glu	Leu	35	40	45	
His	Pro	Leu	Asn	Ala	His	Ser	Gly	Asn	Lys	Ala	Asp	Phe	Gln	Arg	Ser	50	55	60	
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Met	Thr	Val	Leu	Pro	Ala	Lys	Ala	Ser	Glu	Val	Asn	Leu	Glu	Glu	Leu	85	90	95	
Pro	Pro	Leu	Asn	Tyr	Phe	Leu	His	Ala	Phe	Tyr	Tyr	Ser	Trp	Tyr	Gly	100	105	110	
Asn	Pro	Gln	Phe	Asp	Gly	Lys	Tyr	Ile	His	Trp	Asn	His	Pro	Val	Leu	115	120	125	
Glu	His	Trp	Asp	Pro	Arg	Ile	Ala	Lys	Asn	Tyr	Pro	Gln	Gly	Gln	His	130	135	140	
Ser	Pro	Pro	Asp	Asp	Ile	Gly	Ser	Ser	Phe	Tyr	Pro	Glu	Leu	Gly	Ser	145	150	155	160
Tyr	Ser	Ser	Arg	Asp	Pro	Ser	Val	Ile	Glu	Thr	His	Met	Lys	Gln	Met	165	170	175	
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Pro	Tyr	Ser	Asn	Arg	Asp	Asp	Gln	Asn	Met	His	Gln	Asn	Ile	Lys	Tyr	225	230	235	240
Ile	Ile	Asp	Lys	Tyr	Gly	Asn	His	Pro	Ala	Phe	Tyr	Arg	Tyr	Lys	Thr	245	250	255	
Arg	Thr	Gly	His	Ser	Leu	Pro	Met	Phe	Tyr	Val	Tyr	Asp	Ser	Tyr	Ile	260	265	270	
Thr	Lys	Pro	Thr	Ile	Trp	Ala	Asn	Leu	Leu	Thr	Pro	Ser	Gly	Ser	Gln	275	280	285	

Ser Val Arg Ser Ser Leu Tyr Asp Gly Leu Phe Ile Ala Leu Leu Val
 290 295 300

Glu Glu Lys His Lys Asn Asp Ile Leu Gln Ser Gly Phe Asp Gly Ile
 305 310 315 320

Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly Ser Ser His Gln
 325 330 335

Asn Trp Asn Asn Leu Lys Ser Phe Cys Glu Lys Asn Asn Leu Met Phe
 340 345 350

Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr Ser Ile Arg Pro Trp
 355 360 365

Asn Thr Gln Asn Thr Arg Asn Arg Val Asn Gly Lys Tyr Tyr Glu Val
 370 375 380

Gly Leu Ser Ala Ala Leu Gln Thr His Pro Ser Leu Ile Ser Ile Thr
 385 390 395 400

Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu Lys Ala Val Pro
 405 410 415

Lys Arg Thr Ala Asn Thr Ile Tyr Leu Asp Tyr Arg Pro His Lys Pro
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<223> Description of Artificial Sequence: Synthetic primer

<400> 18

gaattccctg aagcaggcag ctgttgatcc

30

<210> 19

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 19

aatttatgga ctacaaggat gacgacgaca agg

33

<210> 20

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 20

aattccttgt cgtcgatcatc cttgtagtcc ata

33

<210> 21

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 21

ggcgcgccga cttccaaagg agtgatcgaa tcgacatgg

39

<210> 22

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 22

ccttaattaa ttatgaagca ggcagctggt gatccaatgc

40

<210> 23

<211> 290

<212> PRT

<213> Rattus norvegicus

<400> 23

Met Lys Gln Met Arg Ser Ala Ser Ile Gly Val Leu Ala Leu Ser Trp
1 5 10 15Tyr Pro Pro Asp Ala Ser Asp Glu Asn Gly Glu Ala Thr Asp Tyr Leu
20 25 30Val Pro Thr Ile Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val Thr
35 40 45Phe His Ile Glu Pro Tyr Ser Asn Arg Asp Asp Gln Asn Met His Gln
50 55 60Asn Val Lys Tyr Ile Ile Asp Lys Tyr Gly Asn His Pro Ala Phe Tyr
65 70 75 80Arg Tyr Lys Thr Arg Met Gly His Ser Leu Pro Met Phe Tyr Ile Tyr
85 90 95Asp Ser Tyr Ile Thr Lys Pro Lys Thr Trp Ala Asn Leu Leu Thr Pro
100 105 110Ser Gly Ser Gln Ser Val Arg Gly Ser Pro Tyr Asp Gly Leu Phe Ile
115 120 125Ala Leu Leu Val Glu Glu Lys His Lys Tyr Asp Ile Leu Gln Ser Gly
130 135 140Phe Asp Gly Ile Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly
145 150 155 160Ser Ser His Gln Asn Trp Asn Lys Leu Lys Ser Phe Cys Glu Lys Asn
165 170 175Asn Met Ile Phe Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr Ser
180 185 190Ile Arg Pro Trp Asn Thr Gln Asn Thr Arg Asn Arg Ile Asn Gly Lys
195 200 205

Tyr Tyr Glu Val Gly Leu Ser Ala Ala Leu Gln Thr Gln Pro Ser Leu
 210 215 220
 Ile Ser Ile Thr Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu
 225 230 235 240
 Lys Ala Val Pro Lys Arg Thr Ala Asn Thr Val Tyr Leu Asp Tyr Arg
 245 250 255
 Pro His Lys Pro Ser Leu Tyr Leu Glu Ile Thr Arg Lys Trp Ser Glu
 260 265 270
 Lys Tyr Ser Lys Glu Arg Met Thr Tyr Ala Leu Asp Gln Gln Leu Pro
 275 280 285
 Ala Ser
 290

<210> 24
 <211> 290
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Arg Gln Met Arg Ser Ala Ser Ile Gly Val Leu Ala Leu Ser Trp
 1 5 10 15
 Tyr Pro Pro Asp Val Asn Asp Glu Asn Gly Glu Pro Thr Asp Asn Leu
 20 25 30
 Val Pro Thr Ile Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val Thr
 35 40 45
 Phe His Ile Glu Pro Tyr Ser Asn Arg Asp Asp Gln Asn Met Tyr Lys
 50 55 60
 Asn Val Lys Tyr Ile Ile Asp Lys Tyr Gly Asn His Pro Ala Phe Tyr
 65 70 75 80
 Arg Tyr Lys Thr Lys Thr Gly Asn Ala Leu Pro Met Phe Tyr Val Tyr
 85 90 95
 Asp Ser Tyr Ile Thr Lys Pro Glu Lys Trp Ala Asn Leu Leu Thr Thr
 100 105 110
 Ser Gly Ser Arg Ser Ile Arg Asn Ser Pro Tyr Asp Gly Leu Phe Ile
 115 120 125
 Ala Leu Leu Val Glu Glu Lys His Lys Tyr Asp Ile Leu Gln Ser Gly
 130 135 140
 Phe Asp Gly Ile Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly
 145 150 155 160

Ser Ser His Gln Asn Trp Ala Ser Leu Lys Leu Phe Cys Asp Lys Tyr
 165 170 175
 Asn Leu Ile Phe Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr Ser
 180 185 190
 Ile Arg Pro Trp Asn Thr Gln Asn Thr Arg Asn Arg Ile Asn Gly Lys
 195 200 205
 Tyr Tyr Glu Ile Gly Leu Ser Ala Ala Leu Gln Thr Arg Pro Ser Leu
 210 215 220
 Ile Ser Ile Thr Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu
 225 230 235 240
 Lys Ala Val Pro Lys Arg Thr Ser Asn Thr Val Tyr Leu Asp Tyr Arg
 245 250 255
 Pro His Lys Pro Gly Leu Tyr Leu Glu Leu Thr Arg Lys Trp Ser Glu
 260 265 270
 Lys Tyr Ser Lys Glu Arg Ala Thr Tyr Ala Leu Asp Arg Gln Leu Pro
 275 280 285
 Val Ser
 290

<210> 25
 <211> 195
 <212> PRT
 <213> Homo sapiens

<400> 25

Met Ala Lys Phe Arg Arg Arg Thr Cys Ile Ile Leu Ala Leu Phe Ile
 1 5 10 15
 Leu Phe Ile Phe Ser Leu Met Met Gly Leu Lys Met Leu Arg Pro Asn
 20 25 30
 Thr Ala Thr Phe Gly Ala Pro Phe Gly Leu Asp Leu Leu Pro Glu Leu
 35 40 45
 His Gln Arg Thr Ile His Leu Gly Lys Asn Phe Asp Phe Gln Lys Ser
 50 55 60
 Asp Arg Ile Asn Ser Glu Thr Asn Thr Lys Asn Leu Lys Ser Val Glu
 65 70 75 80
 Ile Thr Met Lys Pro Ser Lys Ala Ser Glu Leu Asn Leu Asp Glu Leu
 85 90 95

Pro Pro Leu Asn Asn Tyr Leu His Val Phe Tyr Tyr Ser Trp Tyr Gly
 100 105 110

Asn Pro Gln Phe Asp Gly Lys Tyr Ile His Trp Asn His Pro Val Leu
 115 120 125

Glu His Trp Asp Pro Arg Ile Ala Lys Asn Tyr Pro Gln Gly Arg His
 130 135 140

Asn Pro Pro Asp Asp Ile Gly Ser Ser Phe Tyr Pro Glu Leu Gly Ser
 145 150 155 160

Tyr Ser Ser Arg Asp Pro Ser Val Ile Glu Thr His Met Arg Gln Met
 165 170 175

Arg Ser Ala Ser Ile Gly Val Leu Ala Leu Ser Trp Tyr Pro Pro Asp
 180 185 190

Val Asn Glu
 195

<210> 26

<211> 451

<212> PRT

<213> Rattus norvegicus

<400> 26

Met Gly Ala Leu Met Ala Thr Tyr Ser Glu Gly Met Met Gly Cys Ser
 1 5 10 15

Ser Val Gly Arg Cys Phe Ser Ser Thr Leu Ser Pro Ile Ile Thr Leu
 20 25 30

Val Ala Thr Ser Met Lys Ser Thr Pro Arg Val Leu Glu Asn Lys Ala
 35 40 45

Asp Phe Gln Arg Ser Asp Arg Ile Asp Met Glu Thr Asn Thr Lys Asp
 50 55 60

Leu Lys Gly Ala Gly Val Thr Val His Pro Pro Arg Ala Ser Glu Val
 65 70 75 80

Asn Leu Glu Glu Leu Pro Pro Leu Asn Tyr Phe Val His Ala Phe Tyr
 85 90 95

Tyr Ser Trp Tyr Gly Asn Pro Gln Phe Asp Gly Lys Tyr Val His Trp
 100 105 110

Asn His Pro Val Leu Glu His Trp Asp Pro Arg Ile Ala Lys Asn Tyr
 115 120 125

Pro Gln Gly Arg His Ser Pro Pro Asp Asp Ile Gly Ser Ser Phe Tyr
 130 135 140

Pro	Glu	Leu	Gly	Ser	Tyr	Ser	Ser	Arg	Asp	Pro	Ser	Val	Ile	Glu	Thr	
145					150					155					160	
His	Met	Lys	Gln	Met	Arg	Ser	Ala	Ser	Ile	Gly	Val	Leu	Ala	Leu	Ser	
				165					170					175		
Trp	Tyr	Pro	Pro	Asp	Ala	Ser	Asp	Glu	Asn	Gly	Glu	Ala	Thr	Asp	Tyr	
			180					185					190			
Leu	Val	Pro	Thr	Ile	Leu	Asp	Lys	Ala	His	Lys	Tyr	Asn	Leu	Lys	Val	
		195					200					205				
Thr	Phe	His	Ile	Glu	Pro	Tyr	Ser	Asn	Arg	Asp	Asp	Gln	Asn	Met	His	
	210					215					220					
Gln	Asn	Val	Lys	Tyr	Ile	Ile	Asp	Lys	Tyr	Gly	Asn	His	Pro	Ala	Phe	
225					230					235					240	
Tyr	Arg	Tyr	Lys	Thr	Arg	Met	Gly	His	Ser	Leu	Pro	Met	Phe	Tyr	Ile	
			245						250					255		
Tyr	Asp	Ser	Tyr	Ile	Thr	Lys	Pro	Lys	Thr	Trp	Ala	Asn	Leu	Leu	Thr	
			260					265					270			
Pro	Ser	Gly	Ser	Gln	Ser	Val	Arg	Gly	Ser	Pro	Tyr	Asp	Gly	Leu	Phe	
		275					280					285				
Ile	Ala	Leu	Leu	Val	Glu	Glu	Lys	His	Lys	Tyr	Asp	Ile	Leu	Gln	Ser	
	290					295					300					
Gly	Phe	Asp	Gly	Ile	Tyr	Thr	Tyr	Phe	Ala	Thr	Asn	Gly	Phe	Thr	Tyr	
305					310					315					320	
Gly	Ser	Ser	His	Gln	Asn	Trp	Asn	Lys	Leu	Lys	Ser	Phe	Cys	Glu	Lys	
			325					330						335		
Asn	Asn	Met	Ile	Phe	Ile	Pro	Ser	Val	Gly	Pro	Gly	Tyr	Ile	Asp	Thr	
		340						345					350			
Ser	Ile	Arg	Pro	Trp	Asn	Thr	Gln	Asn	Thr	Arg	Asn	Arg	Ile	Asn	Gly	
		355					360					365				
Lys	Tyr	Tyr	Glu	Val	Gly	Leu	Ser	Ala	Ala	Leu	Gln	Thr	Gln	Pro	Ser	
	370					375					380					
Leu	Ile	Ser	Ile	Thr	Ser	Phe	Asn	Glu	Trp	His	Glu	Gly	Thr	Gln	Ile	
385					390				395						400	
Glu	Lys	Ala	Val	Pro	Lys	Arg	Thr	Ala	Asn	Thr	Val	Tyr	Leu	Asp	Tyr	
			405					410					415			
Arg	Pro	His	Lys	Pro	Ser	Leu	Tyr	Leu	Glu	Ile	Thr	Arg	Lys	Trp	Ser	
		420						425					430			

Glu Lys Tyr Ser Lys Glu Arg Met Thr Tyr Ala Leu Asp Gln Gln Leu
 435 440 445

Pro Ala Ser
 450

<210> 27
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide motif

<220>
 <221> MOD_RES
 <222> (4)
 <223> Lys or Arg

<400> 27
 Asp Phe Gln Xaa Ser Asp Arg Ile Asn
 1 5

<210> 28
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 28
 His Asp Glu Leu
 1

<210> 29
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 29
 Lys Asp Glu Leu
 1